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     (FILE 'HOME' ENTERED AT 17:54:57 ON 07 MAR 2002)

     FILE 'REGISTRY' ENTERED AT 17:55:05 ON 07 MAR 2002
L*** DEL      0 S PTSH/CN

     FILE 'HCAPLUS' ENTERED AT 17:55:17 ON 07 MAR 2002
L1          157 SEA ABB=ON  PLU=ON  PTSH
L2         1160 SEA ABB=ON  PLU=ON  CORYNEBACTERIA OR CORYNEBACTERIA GLUTAMICUM
                 OR (BACTERIA (L) CORYNEFORM)
L3            1 SEA ABB=ON  PLU=ON  L1 (L) L2
                D IBIB AB 1
L4           33 SEA ABB=ON  PLU=ON  L1 (L) (DNA OR CDNA OR NUCLEIC ACID OR
                POLYNUCLEOTIDE)
L5           31 SEA ABB=ON  PLU=ON  L4 AND PD<20000113
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=> d ibib ab 1

L3 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:523505 HCAPLUS
DOCUMENT NUMBER: 135:121253
TITLE: The ptsH gene of Corynebacterium glutamicum and its use in increasing yields of lysine in fermentation
INVENTOR(S): Farwick, Mike; Moeckel, Bettina; Pfefferle, Walter
PATENT ASSIGNEE(S): Degussa A.-G., Germany
SOURCE: Ger. Offen., 10 pp.
CODEN: GWXXBX
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 10001101	A1	20010719	DE 2000-10001101	20000113
EP 1118666	A2	20010725	EP 2001-100695	20010112
EP 1118666	A3	20010816		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2001224390	A2	20010821	JP 2001-5671	20010112
CN 1319667	A	20011031	CN 2001-100614	20010112

PRIORITY APPLN. INFO.: DE 2000-10001101 A 20000113

AB The **ptsH** gene of Corynebacterium glutamicum ATCC13032 encoding component H of the phosphotransferase system is cloned and characterized for use in increasing the efficiency of fermn. of lysine by **coryneform bacteria**. The gene was identified by querying a C. glutamicum sequence database for homologs of known **ptsH** genes. Diruption of the gene increased the yield of lysine in a Corynebacterium host from 9.54 g lysine/L at 13.1 OD660 to 12.29 g lysine/L at 12.7 OD660.

=> d ibib ab 1-31

L5 ANSWER 1 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:799234 HCAPLUS
DOCUMENT NUMBER: 135:836
TITLE: Regulation of the pts operon in low G+C Gram-positive bacteria
AUTHOR(S): Vadeboncoeur, Christian; Frenette, Michel; Lortie, Louis-Andre
CORPORATE SOURCE: Groupe de recherche en ecologie buccale (GREB), Departement de biochimie et de microbiologie, Faculte des sciences et de genie, and Faculte de medecine dentaire, Universite Laval, Sainte-Foy, QC, G1K 7P4, Can.
SOURCE: J. Mol. Microbiol. Biotechnol. (**2000**), 2(4), 483-490
CODEN: JMMBFF; ISSN: 1464-1801
PUBLISHER: Horizon Scientific Press
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review with 54 refs. The sugar transport system called phosphoenolpyruvate: sugar phosphotransferase (PTS) is widespread among eubacteria. Its is generally composed of two cytoplasmic proteins, HPr and EI, which are found in all bacteria possessing a PTS, and a family of Ells whose no., specificity, and mol. structure in terms of domain arrangement vary from species to species. In low G+C Gram-pos. bacteria, the genes coding for the general proteins HPr and EI, designated **ptsH** and ptsI resp., are organized into the pts operon. In this paper, we summarize current knowledge about the regulation of the pts operon in low G+C Gram-pos. bacteria. Physiol. data indicate that EI and most particularly HPr make up a substantial proportion of cellular proteins. Their synthesis is not coordinated and is influenced by environmental factors. The principal **DNA** cis-elements involved in the regulation of pts operon transcription are a strong promoter whose sequence and structure are very similar to those of the canonical promoter recognized by the Escherichia coli and Bacillus subtilis major RNA polymerases, a 5'-untranslated region, a rhodependent terminator located at the 5' end of pstI, and an intrinsic terminator located downstream from ptsI. Anal. of **ptsH** and ptsI Shine-Dalgarno sequences as well as exptl. results obtained with a Streptococcus salivarius mutant suggest that the expression of HPr and EI is also controlled at the translation level.
REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:721560 HCAPLUS
DOCUMENT NUMBER: 132:61424
TITLE: Transposon-induced mutations in two loci of Listeria monocytogenes serotype 1/2a result in phage resistance and lack of N-acetylglucosamine in the teichoic acid of the cell wall
AUTHOR(S): Tran, Huyen L.; Fiedler, F.; Hodgson, D. A.; Kathariou, S.
CORPORATE SOURCE: Department of Microbiology, University of Hawaii, Honolulu, HI, 96822, USA
SOURCE: Appl. Environ. Microbiol. (**1999**), 65(11), 4793-4798
CODEN: AEMIDF; ISSN: 0099-2240
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Teichoic acid-assocd. N-acetylglucosamine and rhamnose have been shown to serve as phage receptors in Listeria monocytogenes serotype 1/2a. We generated and characterized two single-copy Tn916.DELTA.E mutants which were resistant to phage A118 and several other serotype 1/2a-specific phages. In one mutant the insertion was immediately upstream of the

recently identified ptsHI locus, which encodes two proteins of the phosphoenolpyruvate-dependent carbohydrate uptake system, whereas in the other the insertion was immediately upstream of an operon whose most distal gene was clpC, involved in stress responses and virulence. Transduction expts. confirmed the assocn. of the phage-resistant phenotype of these mutants with the transposon insertion. Phage A118 resistance of the mutants could be attributed to inability of the phage to absorb onto the mutant cells, and biochem. anal. of cell wall compn. showed that the teichoic acids of both mutants were deficient in N-acetylglucosamine. Rhamnose and other teichoic acid and cell wall components were not affected.

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 3 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:707164 HCAPLUS
DOCUMENT NUMBER: 132:59899
TITLE: Phosphocarrier proteins in an intracellular symbiotic bacterium of aphids
AUTHOR(S): Matsumoto, Kyoko; Morioka, Mizue; Ishikawa, Hajime
CORPORATE SOURCE: Department of Biological Sciences, Graduate School of Science, The University of Tokyo, Tokyo, 113-0033, Japan
SOURCE: J. Biochem. (Tokyo) (**1999**), 126(3), 578-583
CODEN: JOBIAO; ISSN: 0021-924X
PUBLISHER: Japanese Biochemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A GroEL homolog produced by Buchnera, an intracellular symbiotic bacterium of aphids, is not only a mol. chaperone but also a novel phosphocarrier protein, suggesting that this protein plays a role in a signal transducing system specific to bacteria living in an intracellular environment. This prompted us to look into phosphocarrier proteins of Buchnera that may be shared in common with other bacteria. As a result, no evidence was obtained for the presence of sensor kinases of the two-component system in Buchnera, which are found in many bacteria. It is possible that the lack of sensor kinases is compensated for by the multifunctional GroEL homolog in this symbiotic bacteria. In contrast, we successfully identified three phosphotransferase system genes, ptsH, ptsI, and crr in Buchnera, and provide evidence for their active expression. While the deduced amino acid sequences of these gene products, histidine-contg. phosphocarrier protein, Enzyme I, and Enzyme III were similar to their counterparts in Escherichia coli, the predicted isoelec. points of the Buchnera proteins were strikingly higher. It was also suggested that Buchnera Enzyme I, when produced in E. coli, is able to accept the phosphoryl group from phosphoenolpyruvate, but not from ATP.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 4 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:656723 HCAPLUS
DOCUMENT NUMBER: 131:348883
TITLE: The phosphotransferase system (PTS) of Streptomyces coelicolor identification and biochemical analysis of a histidine phosphocarrier protein HPr encoded by the gene ptsH
AUTHOR(S): Parche, Stephan; Schmid, Roland; Titgemeyer, Fritz
CORPORATE SOURCE: Lehrstuhl fur Mikrobiologie, Friedrich-Alexander-Universitat Erlangen-Nurnberg, Erlangen, D-91058, Germany
SOURCE: Eur. J. Biochem. (**1999**), 265(1), 308-317
CODEN: EJBCAI; ISSN: 0014-2956
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB HPr, the histidine-contg. phosphocarrier protein of the bacterial phosphotransferase system (PTS) controls sugar uptake and carbon

utilization in low-GC Gram-pos. bacteria and in Gram-neg. bacteria. We have purified HPr from Streptomyces coelicolor cell exts. The N-terminal sequence matched the product of an S. coelicolor orf, designated ptsH, sequenced as part of the S. coelicolor genome sequencing project. The ptsH gene appears to form a monocistronic operon. Detn. of the evolutionary relationship revealed that S. coelicolor HPr is equally distant to all known HPr and HPr-like proteins. The presumptive phosphorylation site around histidine 15 is perfectly conserved while a second possible phosphorylation site at serine 47 is not well-conserved. HPr was overproduced in Escherichia coli in its native form and as a histidine-tagged fusion protein. Histidine-tagged HPr was purified to homogeneity. HPr was phosphorylated by its own enzyme I (EI) and heterologously phosphorylated by EI of Bacillus subtilis and Staphylococcus aureus, resp. This phosphoenolpyruvate-dependent phosphorylation was absent in an HPr mutant in which histidine 15 was replaced by alanine. Reconstitution of the fructose-specific PTS demonstrated that HPr could efficiently phosphorylate enzyme IIFructose. HPr-P could also phosphorylate enzyme IIGlucose of B. subtilis, enzyme IILactose of S. aureus, and IIAMannitol of E. coli. ATP-dependent phosphorylation was detected with HPr kinase/phosphatase of B. subtilis. These results present the first identification of a gene of the PTS complement of S. coelicolor, providing the basis to elucidate the role(s) of HPr and the PTS in this class of bacteria.

REFERENCE COUNT: 62 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 5 OF 31 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:484000 HCAPLUS
DOCUMENT NUMBER: 131:282865
TITLE: Analysis of a ptsH homologue from Streptomyces coelicolor A3(2)
AUTHOR(S): Butler, Michael J.; Deutscher, Josef; Postma, Pieter W.; Wilson, T. J. Greer; Galinier, Anne; Bibb, Mervyn J.
CORPORATE SOURCE: Department of Genetics, John Innes Centre, Colney, Norwich, UK
SOURCE: FEMS Microbiol. Lett. (**1999**), 177(2), 279-288
CODEN: FMLED7; ISSN: 0378-1097
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A ptsH homolog of Streptomyces coelicolor A3(2) was identified in the emerging genome sequence, cloned in Escherichia coli and the S. coelicolor HPr over-produced and purified. The protein was phosphorylated in vitro in a phosphoenolpyruvate (PEP)-dependent manner by purified enzyme I (EI) from Bacillus subtilis, and much less efficiently in an ATP-dependent manner by purified HPr kinase, also from B. subtilis. There was no indication of ATP-dependent phosphorylation of the purified protein by cell exts. of either S. coelicolor or Streptomyces lividans. Deletion of the ptsH homolog from the S. coelicolor and S. lividans chromosomes had no effect on growth when fructose was supplied as sole carbon source, and in S. coelicolor it had no effect on glucose repression of agarase and galactokinase synthesis, suggesting that the HPr encoded by this gene does not play an essential role in fructose transport nor a general role in carbon catabolite repression.

REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 6 OF 31 HCAPLUS COPYRIGHT 2002 ACS

ACCESSION NUMBER: 1999:238609 HCAPLUS
DOCUMENT NUMBER: 131:2762
TITLE: Studies on somatic embryogenesis in asparagus
AUTHOR(S): Saito, Takeo
CORPORATE SOURCE: Dep. Res. Planning Coordination, Natl. Res. Inst. Vegetables, Ornamental Plants and Tea, 360 Kusawa, Ano, Mie, 514-2392, Japan

SOURCE: Yasai, Chagyo Shikenjo Kenkyu Hokoku (**1999**), 14, 105-164
CODEN: YCSHFM; ISSN: 1343-2206
PUBLISHER: Norin Suisansho Yasai, Chagyo Shikenjo
DOCUMENT TYPE: Journal; General Review
LANGUAGE: Japanese

AB A review with many refs. Highly efficient somatic embryogenesis in asparagus and eggplant can be achieved from suspension cultures by elevating the concn. of gelrite in the regeneration medium in combination with an aseptic ventilative filter as a capping material of the culture vessel. Somatic embryos cultured for longer period tended to show higher germination rate. The polypeptide profiles of the somatic embryos in the later stage became similar to those of mature zygotic embryos, suggesting the metabolic change from immature to mature state. A 17.5 kDa polypeptide may be assocd. with maturation or prepn. for germination of asparagus embryos. Differences in mRNA populations between somatic embryos cultured under desiccated and wet conditions were examd. by the differential display method. One of the clones, pTSD01a, shared similarity with retrotransposon Tha1-2 integrase motif of Nicotiana alata. Moreover, a **cDNA** encoding a homolog of phosphoenolpyruvate: sugar phosphotransferase system H (**ptsH**) was isolated.

L5 ANSWER 7 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:663232 HCAPLUS
DOCUMENT NUMBER: 130:33754
TITLE: Suppression of the **ptsH** mutation in Escherichia coli and Salmonella typhimurium by a **DNA** fragment from Lactobacillus casei
AUTHOR(S): Monedero, Vicente; Postma, Pieter W.; Perez-Martinez, Gaspar
CORPORATE SOURCE: Departamento de Biotecnologia, Instituto de Agroquimica Tecnologia de Alimentos, Valencia, 46100, Spain
SOURCE: J. Bacteriol. (**1998**), 180(19), 5247-5250
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A **DNA** fragment from Lactobacillus casei that restores growth to Escherichia coli and Salmonella typhimurium **ptsH** mutants on glucose and other substrates of the phosphoenolpyruvate:carbohydrate phosphotransferase system (PTS) has been isolated. These mutants lack the HPr protein, a general component of the PTS. Sequencing of the cloned fragment revealed the absence of **ptsH** homologues. Instead, the complementation ability was located in a 120-bp fragment that contained a sequence homolog to the binding site of the Cra regulator from enteric bacteria. Expts. indicated that the reversion of the **ptsH** phenotype was due to a titrn. of the Cra protein, which allowed the constitutive expression of the fructose operon.

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 8 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1998:602019 HCAPLUS
DOCUMENT NUMBER: 129:311571
TITLE: Cloning and expression of the Listeria monocytogenes Scott A ptsH and ptsI genes, coding for HPr and enzyme I, respectively, of the phosphotransferase system
AUTHOR(S): Christensen, Douglas P.; Benson, Andrew K.; Hutkins, Robert W.
CORPORATE SOURCE: School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE, 68583-0919, USA
SOURCE: Appl. Environ. Microbiol. (**1998**), 64(9), 3147-3152
CODEN: AEMIDF; ISSN: 0099-2240
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal

LANGUAGE: English

AB The phosphoenolpyruvate (PEP)-dependent phosphotransferase system (PTS) utilizes high-energy phosphate present in PEP to drive the uptake of several different carbohydrates in bacteria. In order to examine the role of the PTS in the physiol. of Listeria monocytogenes, the authors identified the ptsH and ptsI genes encoding the HPr and enzyme I proteins, resp., of the PTS. Nucleotide sequence anal. indicated that the predicted proteins are nearly 70% similar to HPr and enzyme I proteins from other organisms. Purified L. monocytogenes HPr overexpressed in Escherichia coli was also capable of complementing an HPr defect in heterologous exts. of Staphylococcus aureus ptsH mutants. Addnl. studies of the transcriptional organization and control indicated that the ptsH and ptsI genes are organized into a transcription unit that is under the control of a consensus-like promoter and that expression of these genes is mediated by glucose availability and pH or by byproducts of glucose metab.

L5 ANSWER 9 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1996:131388 HCAPLUS
DOCUMENT NUMBER: 124:280531
TITLE: Cloning and characterization of the Bacillus subtilis prkA gene encoding a novel serine protein kinase
AUTHOR(S): Fischer, Cecile; Geourjon, Christophe; Bourson, Claude; Deutscher, Josef
CORPORATE SOURCE: Institut de Biologie et Chimie des Proteines, CNRS, Lyon, F-69367, Fr.
SOURCE: Gene (**1996**), 168(1), 55-60
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We have cloned and sequenced a 3574-bp Bacillus subtilis (Bs) **DNA** fragment located between the nrdA and citB genes at about 169.degree. on the chromosome. An Escherichia coli strain, LBG1605, carrying a mutated **ptsH** gene (encoding HPr (His-contg. protein) of the bacterial phosphotransferase system (PTS)) and complemented for PTS activity with the **ptsH** of Staphylococcus carnosus, exhibited reduced mannitol fermn. activity when transformed with a plasmid bearing this 3574-bp Bs fragment. This fragment contained an incomplete and two complete open reading frames (ORFs). The product of the first complete ORF, a protein composed of 235 amino acids (aa) (25038 Da), was found to be responsible for the obsd. reduced mannitol fermn. The 3' part of this 705-bp second ORF and the 428-bp incomplete first ORF encode aa sequences exhibiting almost 40% sequence identity. However, the function of these two proteins remains unknown. The third ORF, the 1893-bp prkA gene, encodes a protein (PrkA) of 72889 Da. PrkA possesses the A-motif of nucleotide-binding proteins and exhibits distant homol. to eukaryotic protein kinases. Several of the essential aa in the loops known to form the active site of cyclic adenosine 3',5'-monophosphate (cAMP)-dependent protein kinase appeared to be conserved in PrkA. After expression of prkA and purifn. of PrkA, we could demonstrate that PrkA can indeed phosphorylate a Bs 60-kDa protein at a Ser residue.

L5 ANSWER 10 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:209992 HCAPLUS
DOCUMENT NUMBER: 120:209992
TITLE: Promoter switch in the Escherichia coli pts operon
AUTHOR(S): Ryu, Sangryeol; Garges, Susan
CORPORATE SOURCE: Lab. Mol. Biol., Natl. Cancer Inst., Bethesda, MD, 20892, USA
SOURCE: J. Biol. Chem. (**1994**), 269(7), 4767-72
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The ptsH operon of Escherichia coli is controlled by two promoters P0 and P1, each of which is regulated by cAMP receptor protein (CRP) complexed with cAMP (CRP.cntdot.cAMP). The authors have studied the in vitro as well as in vivo transcriptional regulation of these two promoters. Each promoter exhibits a switching mechanism in vitro, where, depending upon

the presence or absence of CRP.cntdot.cAMP, transcription is initiated from different start sites termed a and b. P0 (P0a) is affected by super-coiling: when the template is linear, transcription initiation is switched to a site 3 base pairs upstream (P0b) and becomes more CRP-cAMP dependent. Transcription from the P1 promoter (P1a) switches initiation sites to 7 base pairs downstream (P1b) in the presence of CRP.cntdot.cAMP. Most transcription in vivo was from P1a, and P0b could not be detected in vivo. The results indicate that the two different regulatory mechanisms (one through CRP.cntdot.cAMP, the other through glucose) are working together for fine control of pts expression.

L5 ANSWER 11 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:126393 HCAPLUS
DOCUMENT NUMBER: 120:126393
TITLE: Cloning and sequencing of a cellobiose phosphotransferase system operon from Bacillus stearothermophilus XL-65-6 and functional expression in Escherichia coli
AUTHOR(S): Lai, Xiaokuang; Ingram, L. O.
CORPORATE SOURCE: Dep. Microbiol. Cell Sci., Univ. Florida, Gainesville, FL, 32611, USA
SOURCE: J. Bacteriol. (**1993**), 175(20), 6441-50
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Celluloytic strains of Bacillus stearothermophilus were isolated from nature and screened for the presence of activities assocd. with the degrdn. of plant cell walls. One isolate (strain XL-65-6) which exhibited strong activities with 4-methylumbelliferyl-.beta.-D-glucopyranoside (MUG) and 4-methylumbelliferyl-.beta.-D-cello-biopyranoside (MUC) was used to construct a gene library in Escherichia coli. Clones degrading these model substrates were found to encode the cellobiose-specific genes of the phosphoenolpyruvate-dependent phosphotransferase system (PTS). Both MUG and MUC activities were present together, and both activities were lost concurrently during subcloning expts. A functional E. coli ptsI gene was required for MUC and MUG activities (presumably a **ptsH** gene also). The **DNA** fragment from B. stearothermophilus contained four open reading frames which appear to form a cel operon. Intergenic stop codons for celA, celB, and celC overlapped the ribosomal binding sites of the resp. downstream genes. Frameshift mutations or deletions in celA, celB, and celD were individually shown to result in a loss of MUC and MUG activities. On the basis of amino acid sequence homol. and hydropathy plots of translated sequences, celA and celB were identified as encoding PTS enzyme II and celD was identified as encoding PTS enzyme III. These translated sequences were remarkably similar to their resp. E. coli homologs for cellobiose transport. No reported sequences exhibited a high level of homol. with the celC gene product. The predicted carboxy-terminal region for celC was similar to the corresponding region of E. coli celF, a phospho-.beta.-glucosidase. An incomplete regulatory gene (celR) and proposed promoter sequence were located 5' to the proposed cel operon. A stem-loop resembling a rho-independent terminator was present immediately downstream from celD. These results indicate that B. stearothermophilus XL-65-6 contains a cellobiose-specific PTS for cellobiose uptake. Similar systems may be present in other gram-pos. bacteria.

L5 ANSWER 12 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:102669 HCAPLUS
DOCUMENT NUMBER: 120:102669
TITLE: GTH-cells in the pituitary of the African catfish, Clarias gariepinus, during gonadal maturation: An immunoelectron microscopical study
AUTHOR(S): Zandbergen, M.A.; van den Branden, C.A.V.; Schulz, R.W.; Janssen-Dommerholt, J.; Ruijter, J.M.; Goos, H.J.T.; Peute, J.
CORPORATE SOURCE: Dep. Exp. Zool., Univ. Utrecht, Utrecht, 3584, Neth.
SOURCE: Fish Physiol. Biochem. (**1993**), 11(1-6),

255-263
CODEN: FPBIEP; ISSN: 0920-1742
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In an ultrastructural immunocytochem. study, the authors investigated the development of the gonadotropic cells in the pituitary of two to six months old male African catfish in relation to testicular development. In this period, pituitary and testicular tissue samples were collected on five occasions (groups I-V). Blood samples could only be taken from the fish in groups III-V. The testicular development was divided in three stages, i.e. immature (only spermatogonia, group I), early (spermatogonia and spermatocytes, groups II and III) and advanced (all germ cell stages including spermatozoa, groups IV and V) spermatogenesis. 11-Ketotestosterone blood levels were low, except for the last group. Antisera were raised against the complete catfish .alpha.,.beta.GTH-II, as well as to the sep. .alpha.- and .beta.-subunits of catfish GTH-II. In the proximal pars distalis of immature fish, undifferentiated cells, somatotropes, putative thyrotrops (**pTSH**) and putative gonadotrops (pGTH) were found. In the two latter, secretory granules were labeled with anti-.alpha.GTH, but not with anti-.beta.GTH-II. **PTSH**-and pGTH-cells were distinguished on the basis of the size of their secretory granules. During early spermatogenesis, two classes of putative gonadotrops could be distinguished. One type had the same immunocytochem. and ultrastructural characteristics as in immature fish; the secretory granules in the second cell type, which was more abundant, were also immunopos. for anti-.beta.GTH-II. The mean vol. of the secretory granules in these GTH-II cells was three times larger than that in the early appearing pGTH-cells. In addn., the later appearing GTH-II cells contained large inclusions, known as globules. These structures labeled with anti-.alpha..beta.GTH-II and with anti-.beta.GTH-II, but not with anti-.alpha.GTH. It is assumed that the globules are involved in a differential storage and/or breakdown of the GTH-II subunits. During advanced spermatogenesis, the two gonadotropic cell types could still be distinguished, but the early appearing pGTH-cell type was scarce. The present observations permit the conclusion that the early appearing cells may be GTH-I cells. However, definitive proof about their identity depends on the availability of antibodies or **cDNA** probes specific for GTH-I.

L5 ANSWER 13 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:46978 HCAPLUS
DOCUMENT NUMBER: 120:46978
TITLE: Unique monocistronic operon (ptsH) in Mycoplasma capricolum encoding the phosphocarrier protein, HPr, of the phosphoenolpyruvate:sugar phosphotransferase system. Cloning, sequencing, and characterization of ptsH
AUTHOR(S): Zhu, Peng Peng; Reizer, Jonathan; Reizer, Aiala; Peterkofsky, Alan
CORPORATE SOURCE: Lab. Biochem. Genet., Natl. Heart, Lung, Blood Inst., Bethesda, MD, 20892, USA
SOURCE: J. Biol. Chem. (**1993**), 268(35), 26531-40
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The region of the genome of Mycoplasma capricolum encompassing the gene (**ptsH**) encoding HPr, a general energy-coupling protein of the phosphoenolpyruvate:sugar phosphotransferase system, was cloned and sequenced. Examn. of the sequence revealed a unique arrangement of the **ptsH** gene. In all other bacterial species characterized thus far, the **ptsH** gene is part of a polycistronic operon that includes the gene (ptsI) encoding Enzyme I of the phosphoenolpyruvate:sugar phosphotransferase system; the M. capricolum **ptsH** gene is part of a monocistronic operon that is situated between two open reading frames unrelated to phosphoenolpyruvate:sugar phosphotransferase system function. The gene immediately upstream of **ptsH** codes for a helicase, and the open reading frame immediately downstream of **ptsH**, although

not homologous to any previously identified protein, contains a signature sequence characteristic of [C-5] cytosine-specific **DNA** methylases. The product of the **ptsH** gene has characteristics similar to the HPr protein produced by gram-pos. organisms: it has a greater sequence similarity to HPrs of gram-pos. bacteria than to those of gram-neg. organisms, it is phosphorylated by a protein kinase derived from gram-pos. organisms, and it complements sugar phosphorylation activity in gram-pos. exts. The high calcd. isoelec. point (pI = 9.18) and the absence of glutamate residues in the C-terminal region distinguish the M. capricolum HPr from all previously described HPrs.

L5 ANSWER 14 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:208329 HCAPLUS
DOCUMENT NUMBER: 118:208329
TITLE: Staphylococcal phosphoenolpyruvate-dependent phosphotransferase system: molecular cloning and nucleotide sequence of the Staphylococcus carnosus ptsI gene and expression and complementation studies of the gene product
AUTHOR(S): Kohlbrecher, Detlef; Eisermann, Reinhard; Hengstenberg, Wolfgang
CORPORATE SOURCE: Dep. Microbiol., Ruhr-Univ., Bochum, W-4630/1, Germany
SOURCE: J. Bacteriol. (**1992**), 174(7), 2208-14
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A digoxigenin-labeled **DNA** probe that was complementary to the gene **ptsH** and the beginning of the gene ptsI was used to clone a 3.2-kb HincII-BamHI restriction fragment contg. the complete ptsI gene of S. carnosus. The restriction fragment was cloned in the antisense orientation to the lac promoter in the low-copy-no. vector pSU18. The nucleotide sequences of the ptsI gene, which encodes enzyme I (EC 2.7.3.9), and the corresponding flanking regions were detd. The primary translation product, derived from the nucleotide sequence, consists of 574 amino acids and has a calcd. mol. wt. of 63,369. Amino acid sequence comparison showed 47% similarity to enzyme I of Escherichia coli and 37% similarity to the enzyme I domain of the multiphosphoryl transfer protein of Rhodobacter capsulatus. The histidinyl residue at position 191 could be identified as the probable phosphoenolpyruvate-dependent phosphorylation site of enzyme I of S. carnosus because of sequence homologies with the peptide sequences of enzyme I-active sites of Enterococcus faecalis and Lactococcus lactis. Several in vivo and in vitro complementation studies with the enzyme I ptsI genes of S. carnosus and the E. coli ptsI mutant JLT2 were carried out. The generation times and interaction between enzyme I with histidine-contg. protein from gram-pos. and gram-neg. bacteria were measured in a phosphoryl group transfer test.

L5 ANSWER 15 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1992:606224 HCAPLUS
DOCUMENT NUMBER: 117:206224
TITLE: Evidence for two promoters upstream of the pts operon: Regulation by the cAMP receptor protein regulatory complex
AUTHOR(S): Fox, Donna K.; Presper, Kathleen A.; Adhya, Sankar; Roseman, Saul; Garges, Susan
CORPORATE SOURCE: McCollum-Pratt Inst., Johns Hopkins Univ., Baltimore, MD, 21218, USA
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (**1992**), 89(15), 7056-9
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Several potential target sites for multiple regulatory mechanisms were previously identified in the 5'-flanking region of the pts operon. The authors have investigated the in vitro interactions of the cAMP receptor protein (CRP)-cAMP regulatory complex with two **DNA** binding

sites, by gel mobilized-shift assays, and report the anal. of the functional role of each of the binding sites in vivo. Promoter-reporter gene fusion studies identified two CRP-cAMP-dependent promoters (the previously identified P1 and another promoter, P0) upstream of **ptsH**. The crr promoters (P2) within ptsI may be neg. regulated by CRP-cAMP.

L5 ANSWER 16 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1992:565188 HCAPLUS
DOCUMENT NUMBER: 117:165188
TITLE: Positive regulation of the expression of the Escherichia coli pts operon. Identification of the regulatory regions
AUTHOR(S): De Reuse, H.; Kolb, A.; Danchin, A.
CORPORATE SOURCE: Unite Regul. Expression Genet., Inst. Pasteur, Paris, 75724, Fr.
SOURCE: J. Mol. Biol. (**1992**), 226(3), 623-35
CODEN: JMOBAK; ISSN: 0022-2836
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The pts operon of Escherichia coli is composed of the **ptsH**, ptsI and crr genes coding for three proteins central to the phosphoenolpyruvate-dependent phosphotransferase system (PTS), the HPr, enzyme I and EIIIGlc proteins, resp. It was previously shown that transcription from the promoter region located upstream from the pts operon is regulated by two control circuits, which can occur independently from each other. Transcription of the pts operon is (1) stimulated by the CAP-cAMP complex and (2) enhanced during growth on glucose, a PTS substrate. The **DNA** regions involved in regulation of the expression of the pts operon have been identified. Two promoters, P0 and P1, sepd. by 100 bp are located upstream from the pts operon. In these promoter regions, two sequences were identified that show similarity to the consensus of CAP-binding sites, CAPa located near P0 and CAPb located in the -35 region of P1. In vivo expts. showed that binding of CAP-cAMP at the CAPa site stimulates transcription from the P0 promoter. The binding sites of CAP-cAMP and/or RNA-polymerase on a **DNA** fragment contg. both P0 and P1 promoters as well as both CAPa and CAPb sites were examd. by the technique of DNase I footprinting. These in vitro expts. suggested that CAP-cAMP binding at the CAPb site might also play a role in regulation of the pts operon expression. In addn., it is shown that the **DNA** region carrying the CAPa site is important for regulation by glucose. It is proposed that the expression of the pts operon is controlled by two alternative pos. regulatory mechanisms, which are designed to allow activation of the pts operon under a great variety of growth conditions.

L5 ANSWER 17 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1992:544651 HCAPLUS
DOCUMENT NUMBER: 117:144651
TITLE: Regulation of the sacPA operon of Bacillus subtilis: identification of phosphotransferase system components involved in SacT activity
AUTHOR(S): Arnaud, Maryvonne; Vary, Patricia; Zagorec, Monique; Klier, Andre; Debarbouille, Michel; Postma, Pieter; Rapoport, Georges
CORPORATE SOURCE: Lab. Biochim. Microb., Inst. Pasteur, Paris, 75724, Fr.
SOURCE: J. Bacteriol. (**1992**), 174(10), 3161-70
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The sacT gene which controls the sacPA operon of B. subtilis encodes a polypeptide homologous to the B. subtilis SacY and the Escherichia coli BglG antiterminators. Expression of the sacT gene is shown to be constitutive. The **DNA** sequence upstream from sacP contains a palindromic sequence which functions as a transcriptional terminator. It was previously proposed that SacT acts as a transcriptional

antiterminator, allowing transcription of the sacPA operon. In strains contg. mutations inactivating **ptsH** or ptsI, the expression of sacPA and sacB is constitutive. It is shown here that this constitutivity is due to a fully active SacY antiterminator. In the wild-type sacT+ strain or in the sacT30 mutant, SacT requires both enzyme I and HPr of the phosphotransferase system (PTS) for antitermination. It appears that the PTS exerts different effects on the sacB gene and the sacPA operon. The general proteins of the PTS are not required for the activity of SacY while they are necessary for SacT activity.

L5 ANSWER 18 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1991:444764 HCAPLUS
DOCUMENT NUMBER: 115:44764
TITLE: Staphylococcal phosphoenolpyruvate-dependent phosphotransferase system. Purification and protein sequencing of the Staphylococcus carnosus histidine-containing protein, and cloning and **DNA** sequencing of the **ptsH** gene
AUTHOR(S): Eisermann, Reinhard; Fischer, Roland; Kessler, Ursula; Neubauer, Andrea; Hengstenberg, Wolfgang
CORPORATE SOURCE: Dep. Microbiol., Ruhr-Univ. Bochum, Bochum, W-4630, Fed. Rep. Ger.
SOURCE: Eur. J. Biochem. (**1991**), 197(1), 9-14
CODEN: EJBCAI; ISSN: 0014-2956
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The histidine-contg. protein (HPr) of the bacterial phosphoenolpyruvate-sugar phosphotransferase system (PTS) was isolated from S. carnosus and purified to homogeneity. The protein sequence was detd. by Edman degrdn. of peptides obtained by proteolytic digestion with proteases V8, trypsin, and chem. cleavage with CNBr. Furthermore, immunol. screening of a chromosomal S. carnosus **DNA** gene-library in pUC19 vector enabled S. carnosus HPr-expressing colonies to be isolated. The nucleotide sequence of this **ptsH** gene and its flanking regions was detd. by the dideoxy-chain-termination technique. Upstream, the 264-base pair open reading frame of the **ptsH** gene was flanked by a putative S. carnosus promoter structure and a putative ptsI gene downstream suggesting that **ptsH** gene is the 1st gene in the PTS operon of S. carnosus. Comparison of the amino acid sequence of S. carnosus HPr with the HPr sequence of S. aureus (derived from peptide sequencing) showed a high deg0ee of similarity.

L5 ANSWER 19 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1990:585476 HCAPLUS
DOCUMENT NUMBER: 113:185476
TITLE: The nucleotide sequence of ptsH gene from Klebsiella pneumoniae
AUTHOR(S): Titgemeyer, Friedrich; Eisermann, Reinhard; Hengstenberg, Wolfgang; Lengeler, Joseph W.
CORPORATE SOURCE: Fachbereich Biol./Chem., Univ. Osnabrueck, Osnabrueck, D-4500, Fed. Rep. Ger.
SOURCE: Nucleic Acids Res. (**1990**), 18(7), 1898
CODEN: NARHAD; ISSN: 0305-1048
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The nucleotide sequence of the **ptsH** gene of K. pneumoniae 1033-5P14 strain KAY2026 was detd. Its gene product HPr is involved in carbohydrate uptake and chemotaxis through the phosphoenolpyruvate-dependent carbohydrate:phosphotransferase system (PTS). A 278-bp fragment comprising the whole coding region of the **ptsH** gene was cloned from genomic **DNA** into pUC18. The function was tested by the ability to complement Escherichia coli K12 **ptsH** mutants in sugar fermn. and chemotactical response. The Klebsiella **ptsH** gene has a high homol. to the corresponding genes from E. coli K12 and Salmonella typhimurium. The deduced amino acid sequence shows only an Ile 63 .fwdarw. Leu exchange, indicating that the HPr is a highly conserved protein in closely related enterobacteria.

L5 ANSWER 20 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1990:173155 HCAPLUS
DOCUMENT NUMBER: 112:173155
TITLE: Partial nucleotide sequence of the pts operon in Salmonella typhimurium: comparative analyses in five bacterial genera
AUTHOR(S): Schnierow, B. J.; Yamada, M.; Saier, M. H., Jr.
CORPORATE SOURCE: Dep. Biol., Univ. California, San Diego, CA, 92093, USA
SOURCE: Mol. Microbiol. (**1989**), 3(1), 113-18
CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The nucleotide sequence of a S. typhimurium **DNA** segment of 549 base pairs which encompasses the operator-promoter of the pts operon, the entirety of the **ptsH** gene, encoding HPr of the phosphotransferase system (PTS), the first 29 nucleotides of the ptsI gene, encoding Enzyme I of the PTS, and the intercistronic region between the **ptsH** and ptsI genes was detd. and compared with the corresponding sequence from Escherichia coli. The two sequences showed 91% overall identity, with some regions showing sequence conservation and others exhibiting relative divergence. Two open reading frames were identified in both species. One encoded HPr on the sense strand (255 nucleotides; 12 nucleotide differences, no amino acid differences); the other, on the anti-sense strand, consisted of 291 nucleotides (13 nucleotide differences, 13 amino acid differences). While HPr bears a net neg. charge, the putative protein encoded by the open reading frame on the anti-sense strand is strongly basic. Computer analyses of HPr proteins from five different bacterial genera revealed four regions which show strong sequence identity and therefore are presumed to be crit. for maintenance of biol. activity. Two of these regions were specific to Gram-pos. bacteria. Proposed functions for each of these regions are discussed. Relative evolutionary distances between the HPr proteins were also computed.

L5 ANSWER 21 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1989:567835 HCAPLUS
DOCUMENT NUMBER: 111:167835
TITLE: Thyroid hormone inhibition of human thyrotropin .beta.-subunit gene expression is mediated by a cis-acting element located in the first exon
AUTHOR(S): Wondisford, Fredric E.; Farr, Elizabeth A.; Radovick, Sally; Steinfelder, Hans J.; Moates, J. Michael; McClaskey, John H.; Weintraub, Bruce D.
CORPORATE SOURCE: Mol. Cell. Nutr. Endocrinol. Branch, Natl. Inst. Diabetes Dig. Kidney Dis., Bethesda, MD, 20892, USA
SOURCE: J. Biol. Chem. (**1989**), 264(25), 14601-4
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Thyroid hormone regulation of the human TSH .beta.-subunit gene was examd. in a human embryonal cell line (293). Transient expression studies were performed with chimeric plasmids contg. the reporter gene, chloramphenicol acetyltransferase. Sequences in the first exon between +9 and +37 base pairs (bp) enhanced gene expression from the human TSH.beta. promoter in the absence of thyroid hormone as well as mediated a concn.-dependent triiodothyronine (L-T3) decrease in gene expression. Thyroid hormone inhibition of expression was also conferred to the herpes simplex virus thymidine kinase promoter by inserting +3 to +37 bp of the human TSH.beta. gene downstream from the start of transcription. Primer extension anal. of RNA from transfected cell cultures revealed accurate transcription initiation in only those constructs which contained sequences between +9 and +37 bp. Moreover, RNA anal. confirmed that L-T3 inhibition of chloramphenicol acetyltransferase activity from chimeric **pTSH** .beta.CAT constructs occurred at a pretranslational level. In addn., a nuclear thyroid hormone receptor, c-erbA-.beta., bound to this region in

an avidin-biotin **DNA** binding assay. Thus, L-T3, bound to its receptor, may inhibit human TSH.beta. expression by interfering with an element that functions to enhance gene expression.

L5 ANSWER 22 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1989:111558 HCAPLUS
DOCUMENT NUMBER: 110:111558
TITLE: Evolutionary divergence of enterobacterial genes coding for the glucose phosphotransferase system components
AUTHOR(S): Bouvet, Odile M. M.; Grimont, Patrick A. D.
CORPORATE SOURCE: Unite Enterobact., Inst. Pasteur, Paris, F-75724, Fr.
SOURCE: FEMS Microbiol. Lett. (**1988**), 56(2), 145-9
CODEN: FMLED7; ISSN: 0378-1097
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The **DNA** relatedness of 64 enterobacterial species to Escherichia coli genes ptsI, **ptsH**, crr, ptsG, and ptsLPM was detd. by quant. filter hybridization. **DNA** relatedness was expressed relative to E. coli K-12 **DNA**. Enterobacterial **DNAs** were 0-100% related to E. coli genes and the level of relatedness (except for crr data) reflected the known taxonomic (phylogenetic) position of species with respect to E. coli. When ptsI relatedness data were plotted against **ptsH** data, correlation was excellent. In ptsG vs. ptsLPM plots, the data points (species) were scattered along the diagonal with a large gap sepg. E. coli strains (80-100% relatedness to both probes) from the 63 other species (1-40% relatedness to E. coli genes). Serratia (9 species), Buttiauxella agrestis, and Klebsiella planticola gave higher relatedness values with crr probe than with the other probes tested.

L5 ANSWER 23 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1989:52014 HCAPLUS
DOCUMENT NUMBER: 110:52014
TITLE: **DNA** sequences of the cysK regions of Salmonella typhimurium and Escherichia coli and linkage of the cysK regions to **ptsH**
AUTHOR(S): Byrne, Carolyn R.; Monroe, Robin S.; Ward, Kevin A.; Kredich, Nicholas M.
CORPORATE SOURCE: Div. Anim. Prod., Commonw. Sci. Ind. Res. Organ., Blacktown, 2148, Australia
SOURCE: J. Bacteriol. (**1988**), 170(7), 3150-7
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Nucleotide sequences of the cysK regions of S. typhimurium and E. coli have been detd. A total of 3812 and 2595 nucleotides were sequenced from S. typhimurium and E. coli, resp. Open reading frames of 323 codons were found in both species and were identified as those of cysK by comparison of deduced amino acid sequences with amino- and carboxyl-terminal amino acid analyses of the S. typhimurium cysK gene product O-acetylserine (thiol)-lyase A. The two cysK **DNA** sequences were 85% identical, and the deduced amino acid sequences were 96% identical. The major transcription initiation sites for cysK were found to be virtually identical in the two organisms, by using primer extension and S1 nuclease protection techniques. The -35 region corresponding to the major transcription start site was TTCCCC in S. typhimurium and TTCCGC in E. coli. The deviation of these sequences from the consensus sequence TTGACA may reflect the fact that cysK is subject to pos. control and requires the cysB regulatory protein for expression. Sequences downstream of cysK were found to include **ptsH** and a portion of ptsI, thus establishing the exact relationship of cysK with these two genes. A 290-codon open reading frame, which may represent the cysZ gene, was identified upstream of cysK.

L5 ANSWER 24 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1987:401727 HCAPLUS
DOCUMENT NUMBER: 107:1727

TITLE: Phosphoenolpyruvate:sugar phosphotransferase system of Bacillus subtilis: cloning of the region containing the ptsH and ptsI genes and evidence for a crr-like gene
AUTHOR(S): Gonzy-Treboul, Genevieve; Steinmetz, Michel
CORPORATE SOURCE: Inst. Jacques Monod, Univ. Paris VII, Paris, 75251, Fr.
SOURCE: J. Bacteriol. (**1987**), 169(5), 2287-90
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The genes ptsI and **ptsH**, which encode, resp., enzyme I and Hpr, cytoplasmic proteins involved in the phosphoenolpyruvate:sugar phosphotransferase system, were cloned from B. subtilis. A plasmid contg. a 4.1-kilobase **DNA** fragment was shown to complement Escherichia coli mutations affecting the **ptsH** and ptsI genes. In minicells, this plasmid expressed two proteins with the mol. wts. expected for Hpr and enzyme I. Therefore, **ptsH** and ptsI are adjacent in B. subtilis, as in E. coli. In E. coli, a third gene (crr), involved in glucose translocation and also in catabolite repression, is located downstream from the ptsHI operon. The 4.1-kilobase fragment from B. subtilis was shown to contain a gene that enables an E. coli crr mutant to use glucose. This gene, unlike the E. coli crr gene, was located left of **ptsH**.

L5 ANSWER 25 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1986:585244 HCAPLUS
DOCUMENT NUMBER: 105:185244
TITLE: Cloning and characterization of the cysAMK region of Salmonella typhimurium
AUTHOR(S): Hulanicka, M. Danuta; Garrett, Charles; Jagura-Burdzy, Grazyna; Kredich, Nicholas M.
CORPORATE SOURCE: Howard Hughes Med. Inst., Duke Univ., Durham, NC, 27710, USA
SOURCE: J. Bacteriol. (**1986**), 168(1), 322-7
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A total of 30 kilobases of **DNA** comprising the cysAMK region of S. typhimurium was cloned as a series of fragments in phage .lambda.1059. The genetic organization of this region was established through studies of gene expression from fragments subcloned in pBR322 and from blot hybridization analyses of restriction sites in chromosomal **DNA** from multisite deletion strains. The results give a gene order of cysA-cysM-crr-ptsI-**ptsH**-cysK over a distance of .apprx.12 kilobases. Genes cysM and cysA have been cloned and expressed in pBR322; attempts to obtain stable pBR322 derivs. carrying cysK were unsuccessful.

L5 ANSWER 26 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1985:590639 HCAPLUS
DOCUMENT NUMBER: 103:190639
TITLE: Analysis of the ptsH-ptsI-crr region in Escherichia coli K-12: nucleotide sequence of the ptsH gene
AUTHOR(S): De Reuse, Hilde; Roy, Anne; Danchin, Antoine
CORPORATE SOURCE: Unite Biochim. Regul. Cell., Inst. Pasteur, Paris, 75724, Fr.
SOURCE: Gene (**1985**), 35(1-2), 199-207
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The nucleotide sequence of an E. coli **DNA** segment contg. the **ptsH** gene and the 1st 162 nucleotides of the ptsI gene encoding, resp., Hpr and enzyme I of the phosphoenolpyruvate-dependent glucose phosphotransferase [56941-29-8] system (PTS), was detd. The **ptsH** promoter was localized using the S1 mapping technique. A nucleotide sequence very similar to the consensus binding site for cAMP receptor protein was found in the -35 region of the **ptsH** promoter. The

ptsH gene is transcribed in the same direction as the ptsI gene and the crr gene (encoding enzyme IIIGlc of the PTS). Anal. of the nucleotide sequence substantiates the notion that the **ptsH** -ptsI-crr genes constitute a polycistronic operon.

L5 ANSWER 27 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1985:107255 HCAPLUS
DOCUMENT NUMBER: 102:107255
TITLE: Analysis of the ptsH-ptsI-crr region in Escherichia coli K-12: evidence for the existence of a single transcriptional unit
AUTHOR(S): De Reuse, Hilde; Huttner, Eric; Danchin, Antoine
CORPORATE SOURCE: Unite Biochim. Regul. Cell., Inst. Pasteur, Paris, 75724, Fr.
SOURCE: Gene (**1984**), 32(1-2), 31-40
CODEN: GENED6; ISSN: 0378-1119
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A cosmid contg. the **ptsH**, ptsI, and crr genes of E. coli that code for 3 components of the phosphoenolpyruvate:sugar phosphotransferase [56941-29-8] system (PTS) was isolated. The products of these genes were identified by the maxicell technique. The cloning of the PTS region as a whole allowed the mapping of the **ptsH**, ptsI, and crr genes in a 3.8-kilobase **DNA** fragment, and it was detd. that ptsI and crr are transcribed from a common promoter. Apparently, ptsI and crr constitute a single transcriptional unit, which is likely to include the **ptsH** gene. In addn., the crr gene may have a secondary promoter located inside ptsI.

L5 ANSWER 28 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1984:449408 HCAPLUS
DOCUMENT NUMBER: 101:49408
TITLE: Location and direction of transcription of the ptsH and ptsI genes on the Escherichia coli K12 genome
AUTHOR(S): Britton, P.; Lee, L. G.; Murfitt, D.; Boronat, A.; Jones-Mortimer, M. C.; Kornberg, H. L.
CORPORATE SOURCE: Agric. Res. Counc. Inst. Res. Anim. Dis., Compton, RG16 0NN, UK
SOURCE: J. Gen. Microbiol. (**1984**), 130(4), 861-8
CODEN: JGMIAN; ISSN: 0022-1287
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Recombinant plasmids were constructed that carried various fragments of the **DNA** specifying the E. coli genes **ptsH** and (part of) ptsI, the genes for the common components of the phosphoenolpyruvate:sugar phosphotransferase [56941-29-8]. Expression of plasmid-specified functions in minicells showed the **ptsH** and ptsI were transcribed clockwise. Most of the the transcription of ptsI was from the **ptsH** promoter, but some was from a 2nd site within or after **ptsH**.

L5 ANSWER 29 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1983:138336 HCAPLUS
DOCUMENT NUMBER: 98:138336
TITLE: Phosphotransferase-mediated regulation of carbohydrate utilization in Escherichia coli K12: location of the gsr (tgs) and iex (crr) genes by specialized transduction
AUTHOR(S): Britton, P.; Boronat, A.; Hartley, D. A.; Jones-Mortimer, M. C.; Kornberg, H. L.; Parra, F.; Castle, C.
CORPORATE SOURCE: Dep. Biochem., Univ. Cambridge, Cambridge, CB2 1QW, UK
SOURCE: J. Gen. Microbiol. (**1983**), 129(2), 349-58
CODEN: JGMIAN; ISSN: 0022-1287
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A lysogen of E. coli K12 with .lambda.c857 S7 xis6 nin5 b515 b519

integrated into ptsI was induced and the lysates plated on a Pel- host (on which .lambda. strains with less than the wild-type amt. of **DNA** form plaques at low frequency). All of the 40 plaques examd. contained phage able to transduce .gtoreq.2 of the genes known from bacteriophage P1 transduction expts. to be closely linked to ptsI. Assuming that each specialized transducing phage arose by a single illegitimate recombination event, the distribution of phage types showed that the gene order is cysA gsr ptsI (**ptsH**, iex) cysZ lig; both gsr+ and iex+ were dominant. Anal. of restriction endonuclease digests of the transducing phage confirmed that no unexpected **DNA** rearrangements had taken place and allowed the construction of a map of the sites of action of the restriction endonucleases EcoRI, HindIII, BamI, and Kpn for >20 kilobases of E. coli **DNA**. The cysA and cysZ mutants were deficient in SO42- assimilation.

L5 ANSWER 30 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1977:450052 HCAPLUS
DOCUMENT NUMBER: 87:50052
TITLE: Repression of inducible enzyme synthesis in a mutant of Escherichia coli K12 deleted for the ptsH gene
AUTHOR(S): Gershanovich, V. N.; Ilyina, T. S.; Rusina, O. Y.; Yurovitskaya, N. V.; Bol'shakova, T. N.
CORPORATE SOURCE: N. F. Gamaleya Inst. Epidemiol. Microbiol., Moscow, USSR
SOURCE: Mol. Gen. Genet. (**1977**), 153(2), 185-90
CODEN: MGGEAE
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The genome of .lambda. phage with thermosensitive repressor was inserted into the pts region of the E. coli chromosome. This lysogenic culture possessed the PTS1 phenotype at 30.degree.. A mutant strain with a deletion covering the **ptsH** gene was isolated after a prophage curing procedure. The deletion covered a small fragment of the bacterial genome not extending in the ptsI and lig genes. The isolated .DELTA. **ptsH** mutant possessed all the characteristics of known pts mutants:pleiotropic disturbances of transport and utilization of a number of carbohydrates, repression of the inducible enzyme synthesis, and resistance to glucose catabolite repression. Thus, the phosphorylated form of the heat-stable protein HPr is involved (directly or indirectly) in activation of the **DNA** transcription process.

L5 ANSWER 31 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1977:418886 HCAPLUS
DOCUMENT NUMBER: 87:18886
TITLE: Repression of inducible enzyme synthesis in an Escherichia coli K12 mutant with a ptsH gene deletion defect
AUTHOR(S): Gershanovich, V. N.; Il'ina, T. S.; Rusina, O. Yu.; Yurovitskaya, N. V.; Bol'shakova, T. N.
CORPORATE SOURCE: N. F. Gamaleya Inst. Epidemiol. Microbiol., Moscow, USSR
SOURCE: Mol. Biol. (Moscow) (**1977**), 11(3), 611-19
CODEN: MOBIBO
DOCUMENT TYPE: Journal
LANGUAGE: Russian
AB The genome of .lambda. phage with a thermosensitive repressor was integrated into the pts region of the E. coli chromosome. Such a lysogenic culture behaves as a pts mutant at 30.degree.. Heating of cells of this strain leads to the induction of .lambda. prophage and formation of deletions in the pts region. A mutant with a deletion covering **ptsH** gene was isolated after prophage induction. The deletion nature of the pts mutation was confirmed in genetic and biochem. expts. It was shown that the deletion is small and does not involve ptsI and lig genes. The isolated .DELTA.**ptsH** mutant possesses all the characteristics of pts mutants: pleiotropic impairment of transport and utilization of a no. of carbohydrates, repression of inducible enzyme synthesis, and resistance to catabolite repression by glucose. The

phosphorylated form of HPr may be involved in activation of DNA transcription.

WEST Search History

DATE: Thursday, March 07, 2002

Set Name side by side	Query	Hit Count	Set Name result set
	DB=USPT,PGPB; PLUR=YES; OP=ADJ		
L11	l10 and l7	2	L11
L10	(dna or cdna or nucleic acid or polynucleotide) AND l8	6	L10
L9	l8 and (corynebacteria or corynebacteria glutamicum)	1	L9
L8	Ptsh	14	L8
L7	l6 or l5 or l4 or l3 or l2 or l1	18270	L7
L6	(((536/23.2)!.CCLS.))	3392	L6
L5	(((530/350)!.CCLS.))	6330	L5
L4	(((435/320.1)!.CCLS.))	10584	L4
L3	(((435/252.32)!.CCLS.))	110	L3
L2	(((435/252.3)!.CCLS.))	5229	L2
L1	((435/69.1)!.CCLS.)	7134	L1

END OF SEARCH HISTORY

WEST

End of Result Set

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L9: Entry 1 of 1 File: USPT Nov 13, 2001

US-PAT-NO: 6316232
DOCUMENT-IDENTIFIER: US 6316232 B1

TITLE: Microbial preparation of substances from aromatic metabolism/I

DATE-ISSUED: November 13, 2001

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Sprenger; Georg	Julich			DEX
Siewe; Ruth	Karlsruhe			DEX
Sahm; Hermann	Julich			DEX
Karutz; Martin	Roden			NLX
Sonke; Theodorus	Sittard			NLX

ASSIGNEE-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY	TYPE CODE
Holland Sweetener Company V.O.F.	Geleen			NLX	03
Forschungszentrum Julich GmbH	Julich			DEX	03
DSM Biotech GmbH	Julich			DEX	03

APPL-NO: 9/ 298843 [PALM]
DATE FILED: April 26, 1999

PARENT-CASE:
This is a Continuation of International Appln. No. PCT/NL97/00582 filed Oct. 17, 1997 which designated the U.S.

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	APPL-DATE
DE	196 44 566	October 26, 1996

INT-CL: [7] C12 P 13/04, C12 P 13/22, C12 P 7/22, C12 P 7/04

US-CL-ISSUED: 435/156; 435/106, 435/155, 435/183, 435/108
US-CL-CURRENT: 435/156; 435/106, 435/108, 435/155, 435/183

FIELD-OF-SEARCH: 435/183, 435/106, 435/108, 435/155, 435/156, 536/23.2

PRIOR-ART-DISCLOSED:

U.S. PATENT DOCUMENTS

Search Selected | Search ALL

	PAT-NO	ISSUE-DATE	PATENTEE-NAME	US-CL
☐	5168056	December 1992	Frost et al.	435/172.3

FOREIGN PATENT DOCUMENTS

FOREIGN-PAT-NO	PUBN-DATE	COUNTRY	US-CL
077196	April 1983	EPX	
138526	April 1985	EPX	
145156	June 1985	EPX	
2053906	February 1981	GBX	
19037/1976	February 1976	JPX	
39517/1978	April 1978	JPX	
96/34961	November 1996	WOX	

OTHER PUBLICATIONS

Liao J.C. et al., "Pathway analysis, engineering, and physiological considerations for redirecting central metabolism" Biotechnology and Bioengineering, vol. 52, No. 1, Oct. 5, 1996, pp. 129-140.
Frost J.W. and Drathis K.M., "Biocatalytic syntheses of aromatics from D-glucose: renewable microbial sources of aromatic compounds", Annual Review of Microbiology, vol. 49, 1995, pp. 557-579.
Sprenger G.A. et al., "Transaldolase B of Escherichia coli K-12: cloning of its gene, talB, and characterization of the enzyme from recombinant strains" Journal of Bacteriology, vol. 177, No. 20, Oct. 1995, pp. 5930-5936.
Lu J. -L. and Liao J.C., "Metabolic engineering and control anaylsis for production of aromatics: role of transaldolase" Biotechnology and Bioengineering, vol. 53, No. 2, Jan. 20, 1997, pp. 132-138.
Zhang M. et al., "Metabolic Engineering of a Pentose Metabolism Pathway in Ethanologenic Zymomonas Mobilis", Science, vol. 267, Jan. 13, 1995, pp. 240-243.
Walfridsson M. et al., "Xylose-metabolizing Saccharomyces cerevisiae strains overexpressing the tkl1 and tal1 genes encoding the pentose phosphate pathway enzymes transketolase and transaldolase" Applied and Environmental Microbiology, vol. 61, No. 12, Dec. 1995, pp. 4184-4190.
Berry A., "Improving Production of Aromatic Compounds in Escherichia coli by metabolic engineering" Trends in Biotechnology, vol. 14, No. 7, Jul. 1996, pp. 250-256.
Gosset G. et al., "A direct comparison of approaches for increasing carbon flow to aromatic biosynthesis in Escherichia coli" Journal of Industrial Microbiology, vol. 17, No. 1, Jul. 1996, pp. 47-52.

Weisser P. et al., "Functional expression of the glucose transporter of Zymomonas mobilis leads to restoration of glucose and fructose uptake in Escherichia coli mutants and provides evidence for its facilitator action", Journal of Bacteriology, vol. 177, No. 11, Jun. 1995, pp. 3351-3354.

ART-UNIT: 162
PRIMARY-EXAMINER: Prouty; Rebecca E.
ASSISTANT-EXAMINER: Rao; Manjunath
ATTY-AGENT-FIRM: Pillsbury Winthrop LLP

ABSTRACT:

The invention makes available, by means of an increased provision of intracellular metabolic intermediates, in particular of erythrose 4-phosphate, alternative processes for the microbial preparation of substances, in particular of aromatic amino acids such as L-phenylalanine, in which processes the activity of a transaldolase is increased in a microorganism producing these substances. In preferred embodiments of the invention, the activity of a transketolase or the activity of a transport protein for the PEP-independent uptake of a sugar and/or the activity of a kinase which phosporylates the relevant sugar are/is additionally increased. The invention also relates to gene structures, and to transformed cells carrying these gene structures, which make it possible to implement these processes in a particularly successful manner.

26 Claims, 0 Drawing figures

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Search Results - Record(s) 1 through 6 of 6 returned.

☐ 1. Document ID: US 20020028826 A1

L10: Entry 1 of 6 File: PGPB Mar 7, 2002

PGPUB-DOCUMENT-NUMBER: 20020028826
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020028826 A1

TITLE: HMG-CoA reductase inhibitors and method

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

☐ 2. Document ID: US 20020013334 A1

L10: Entry 2 of 6 File: PGPB Jan 31, 2002

PGPUB-DOCUMENT-NUMBER: 20020013334
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020013334 A1

TITLE: HMG-CoA reductase inhibitors and method

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

☐ 3. Document ID: US 6316232 B1

L10: Entry 3 of 6 File: USPT Nov 13, 2001

US-PAT-NO: 6316232
DOCUMENT-IDENTIFIER: US 6316232 B1

TITLE: Microbial preparation of substances from aromatic metabolism/I

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw Desc | Image

☐ 4. Document ID: US 6248543 B1

L10: Entry 4 of 6 File: USPT Jun 19, 2001

US-PAT-NO: 6248543
DOCUMENT-IDENTIFIER: US 6248543 B1

TITLE: Compositions and methods for screening antimicrobials

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Desc | Image

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☐ 5. Document ID: US 6102690 A

L10: Entry 5 of 6 File: USPT Aug 15, 2000

US-PAT-NO: 6102690
DOCUMENT-IDENTIFIER: US 6102690 A

TITLE: Recombinant organisms capable of fermenting cellobiose

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Desc | Image

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☐ 6. Document ID: US 5948889 A

L10: Entry 6 of 6 File: USPT Sep 7, 1999

US-PAT-NO: 5948889
DOCUMENT-IDENTIFIER: US 5948889 A

TITLE: Compositions and methods for screening antimicrobials

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | Claims | KWIC | Draw. Desc | Image

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(dna or cdna or nucleic acid or polynucleotide) AND l8	6

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Search Results - Record(s) 1 through 10 of 14 returned.

1. Document ID: US 20020028826 A1

L8: Entry 1 of 14 File: PGPB Mar 7, 2002

PGPUB-DOCUMENT-NUMBER: 20020028826
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020028826 A1

TITLE: HMG-CoA reductase inhibitors and method

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

2. Document ID: US 20020013334 A1

L8: Entry 2 of 14 File: PGPB Jan 31, 2002

PGPUB-DOCUMENT-NUMBER: 20020013334
PGPUB-FILING-TYPE: new
DOCUMENT-IDENTIFIER: US 20020013334 A1

TITLE: HMG-CoA reductase inhibitors and method

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

3. Document ID: US 6316232 B1

L8: Entry 3 of 14 File: USPT Nov 13, 2001

US-PAT-NO: 6316232
DOCUMENT-IDENTIFIER: US 6316232 B1

TITLE: Microbial preparation of substances from aromatic metabolism/I

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

4. Document ID: US 6248543 B1

L8: Entry 4 of 14 File: USPT Jun 19, 2001

US-PAT-NO: 6248543
DOCUMENT-IDENTIFIER: US 6248543 B1

TITLE: Compositions and methods for screening antimicrobials

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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☐ 5. Document ID: US 6159738 A

L8: Entry 5 of 14 File: USPT Dec 12, 2000

US-PAT-NO: 6159738
DOCUMENT-IDENTIFIER: US 6159738 A

TITLE: Method for construction of bacterial strains with increased succinic acid production

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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☐ 6. Document ID: US 6102690 A

L8: Entry 6 of 14 File: USPT Aug 15, 2000

US-PAT-NO: 6102690
DOCUMENT-IDENTIFIER: US 6102690 A

TITLE: Recombinant organisms capable of fermenting cellobiose

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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☐ 7. Document ID: US 5948889 A

L8: Entry 7 of 14 File: USPT Sep 7, 1999

US-PAT-NO: 5948889
DOCUMENT-IDENTIFIER: US 5948889 A

TITLE: Compositions and methods for screening antimicrobials

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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☐ 8. Document ID: US 4761685 A

L8: Entry 8 of 14 File: USPT Aug 2, 1988

US-PAT-NO: 4761685
DOCUMENT-IDENTIFIER: US 4761685 A

TITLE: Apparatus and method for solid-state image sensor element registration adjustment

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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☐ 9. Document ID: US 4579898 A

L8: Entry 9 of 14 File: USPT Apr 1, 1986

US-PAT-NO: 4579898
DOCUMENT-IDENTIFIER: US 4579898 A

TITLE: Linear polyethylenes stabilized against melt index drop with aromatic sulfonhydrazides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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☐ 10. Document ID: US 4525487 A

L8: Entry 10 of 14 File: USPT Jun 25, 1985

US-PAT-NO: 4525487
DOCUMENT-IDENTIFIER: US 4525487 A

TITLE: Method for making polyester resin foam by spraying

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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Search Results - Record(s) 11 through 14 of 14 returned.

☐ 11. Document ID: US 4501754 A

L8: Entry 11 of 14 File: USPT Feb 26, 1985

US-PAT-NO: 4501754
DOCUMENT-IDENTIFIER: US 4501754 A

TITLE: Methods of treating bone resorption

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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☐ 12. Document ID: US 4427834 A

L8: Entry 12 of 14 File: USPT Jan 24, 1984

US-PAT-NO: 4427834
DOCUMENT-IDENTIFIER: US 4427834 A

TITLE: Dispersant-VI improver product

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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☐ 13. Document ID: US 4409120 A

L8: Entry 13 of 14 File: USPT Oct 11, 1983

US-PAT-NO: 4409120
DOCUMENT-IDENTIFIER: US 4409120 A

TITLE: Process for forming oil-soluble product

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC
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☐ 14. Document ID: US 4007170 A

L8: Entry 14 of 14 File: USPT Feb 8, 1977

US-PAT-NO: 4007170
DOCUMENT-IDENTIFIER: US 4007170 A

TITLE: Photographic emulsions containing methine dyes having a 1H-imidazo[4,5-b]pyrazine nucleus

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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Search Results - Record(s) 1 through 2 of 2 returned.

☐ 1. Document ID: US 6102690 A

L11: Entry 1 of 2 File: USPT Aug 15, 2000

US-PAT-NO: 6102690
DOCUMENT-IDENTIFIER: US 6102690 A

TITLE: Recombinant organisms capable of fermenting cellobiose

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

☐ 2. Document ID: US 5948889 A

L11: Entry 2 of 2 File: USPT Sep 7, 1999

US-PAT-NO: 5948889
DOCUMENT-IDENTIFIER: US 5948889 A

TITLE: Compositions and methods for screening antimicrobials

Full | Title | Citation | Front | Review | Classification | Date | Reference | Sequences | Attachments | KWIC | Draw Desc | Image

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